

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/704,159

INPUT SET: S13439.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4 (i) APPLICANT: Williams, James A.
5 Thalley, Bruce S.
6
7 (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium
8 Botulinum Neurotoxin
9
10 (iii) NUMBER OF SEQUENCES: 82
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Medlen & Carroll
14 (B) STREET: 220 Montgomery Street, Suite 2200
15 (C) CITY: San Francisco
16 (D) STATE: California
17 (E) COUNTRY: United States of America
18 (F) ZIP: 94104
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Ingolia, Diane E.
33 (B) REGISTRATION NUMBER: 40,027
34 (C) REFERENCE/DOCKET NUMBER: OPHD-02304
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (415) 705-8410
38 (B) TELEFAX: (415) 397-8338
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 24 base pairs
44 (B) TYPE: nucleic acid
45
46

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49 (ii) MOLECULE TYPE: DNA (genomic)
50
51
52
53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55 GGAAATTTAG CTGCAGCATC TGAC
56
57 (2) INFORMATION FOR SEQ ID NO:2:
58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 24 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64
65 (ii) MOLECULE TYPE: DNA (genomic)
66
67
68
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70
71 TCTAGCAAAT TCGCTTGTGT TGAA
72
73 (2) INFORMATION FOR SEQ ID NO:3:
74
75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 20 base pairs
77 (B) TYPE: nucleic acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80
81 (ii) MOLECULE TYPE: DNA (genomic)
82
83
84
85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
86
87 CTCGCATATA GCATTAGACC
88
89 (2) INFORMATION FOR SEQ ID NO:4:
90
91 (i) SEQUENCE CHARACTERISTICS:
92 (A) LENGTH: 19 base pairs
93 (B) TYPE: nucleic acid
94 (C) STRANDEDNESS: single
95 (D) TOPOLOGY: linear
96
97 (ii) MOLECULE TYPE: DNA (genomic)
98
99

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24

20

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100
 101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 19
 102
 103
 104 CTATCTAGGC CTAAAGTAT
 105
 106 (2) INFORMATION FOR SEQ ID NO:5:
 107 (i) SEQUENCE CHARACTERISTICS:
 108 (A) LENGTH: 8133 base pairs
 109 (B) TYPE: nucleic acid
 110 (C) STRANDEDNESS: single
 111 (D) TOPOLOGY: linear
 112
 113 (ii) MOLECULE TYPE: DNA (genomic)
 114
 115
 116 (ix) FEATURE:
 117 (A) NAME/KEY: CDS
 118 (B) LOCATION: 1..8130
 119
 120
 121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: 48
 122
 123 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT
 124 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile
 125 5 10 15
 126 1
 127 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA 96
 128 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu
 129 20 25 30
 130
 131 TAT AAT AAG TTA ACT ACA AAC AAT GAA AAT AAA TAT TTG CAA TTA 144
 132 Tyr Asn Lys Leu Thr Thr Asn Asn Glu Asn Lys Tyr Leu Gln Leu
 133 35 40 45
 134
 135 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT 192
 136 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr
 137 50 55 60
 138
 139 TCA AGC AGA AAT AGA GCA CTC TCT AAT CTA AAA AAA GAT ATA TTA AAA 240
 140 Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys
 141 70 75 80
 142 65
 143 GAA GTA ATT CTT ATT AAA AAT TCC AAT ACA AGC CCT GTA GAA AAA AAT 288
 144 Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn
 145 85 90 95
 146
 147 TTA CAT TTT GTA TGG ATA GGT GGA GAA GTC AGT GAT ATT GCT CTT GAA 336
 148 Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu
 149 100 105 110
 150
 151 TAC ATA AAA CAA TGG GCT GAT ATT AAT GCA GAA TAT ATT AAA CTG 384
 152

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153 Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu
154 115 120 125 432

155 TGG TAT GAT AGT GAA GCA TTC TTA GTA AAT ACA CTA AAA AAG GCT ATA
156 Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile
157 135 140 480

158 145 480

159 GTT GAA TCT TCT ACC ACT GAA GCA TTA CAG CTA CTA GAG GAA GAG ATT
160 Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Glu Ile
161 150 155 160 528

162 145 528

163 CAA AAT CCT CAA TTT GAT AAT ATG AAA TTT TAC AAA AAA AGG ATG GAA
164 Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu
165 165 170 175 576

166 170 576

167 TTT ATA TAT GAT AGA CAA AAA AGG TTT ATA AAT TAT TAT AAA TCT CAA
168 Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln
169 180 185 190 624

170 195 624

171 ATC AAT AAA CCT ACA GTA CCT ACA ATA GAT GAT ATT ATA AAG TCT CAT
172 Ile Asn Lys Pro Thr Val Pro Ile Asp Asp Ile Ile Lys Ser His
173 200 205 672

174 210 672

175 CTA GTA TCT GAA TAT AAT AGA GAT GAA ACT GTA TTA GAA TCA TAT AGA
176 Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg
177 215 220 720

178 220 720

179 ACA AAT TCT TTG AGA AAA ATA AAT AGT AAT CAT GGG ATA GAT ATC AGG
180 Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg
181 230 235 240

182 225 768

183 GCT AAT AGT TTG TTT ACA GAA CAA GAG TTA TTA AAT ATT TAT AGT CAG
184 Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln
185 245 250 255 768

186 260 816

187 GAG TTG TTA AAT CGT GGA AAT TTA GCT GCA GCA TCT GAC ATA GTA AGA
188 Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ser Asp Ile Val Arg
189 265 270 864

190 260 864

191 TTA TTA GCC CTA AAA AAT TTT GGC GGA GTA TAT TTA GAT GTT GAT ATG
192 Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met
193 275 280 285 912

194 290 912

195 CTT CCA GGT ATT CAC TCT GAT TTA TTT AAA ACA ATA TCT AGA CCT AGC
196 Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser
197 295 300 960

198 290 960

199 TCT ATT GGA CTA GAC CGT TGG GAA ATG ATA AAA TTA GAG GCT ATT ATG
200 Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met
201 310 315 320 1008

202 305 1008

203 AAG TAT AAA AAA TAT ATA AAT AAT TAT ACA TCA GAA AAC TTT GAT AAA
204 Lys Tyr Lys Lys Tyr Ile Asn Asn Tyr Thr Ser Glu Asn Phe Asp Lys
205 310 315 320

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206	325	330	335	1056
207	CTT GAT CAA CAA TTA AAA GAT AAT TTT AAA CTC ATT ATA GAA AGT AAA			
208	Leu Asp Gln Gln Leu Lys Asp Asn Phe Lys Leu Ile Ile Glu Ser Lys			
209	340	345	350	
210				
211	AGT GAA AAA TCT GAG ATA TTT TCT AAA TTA GAA AAT TTA AAT GTA TCT			1104
212	Ser Glu Lys Ser Glu Ile Phe Ser Lys Leu Glu Asn Leu Asn Val Ser			
213	355	360	365	
214				
215	GAT CTT GAA ATT AAA ATA GCT TTC GCT TTA GGC AGT GTT ATA AAT CAA			1152
216	Asp Leu Glu Ile Lys Ile Ala Phe Ala Leu Gly Ser Val Ile Asn Gln			
217	370	375	380	
218				
219	GCC TTG ATA TCA AAA CAA GGT TCA TAT CTT ACT AAC CTA GTA ATA GAA			1200
220	Ala Leu Ile Ser Lys Gln Gly Ser Tyr Leu Thr Asn Leu Val Ile Glu			
221	385	390	395	400
222				
223	CAA GTA AAA AAT AGA TAT CAA TTT TTA AAC CAA CAC CTT AAC CCA GCC			1248
224	Gln Val Lys Asn Arg Tyr Gln Phe Leu Asn Gln His Leu Asn Pro Ala			
225	405	410	415	
226				
227	ATA GAG TCT GAT AAT AAC TTC ACA GAT ACT ACT AAA ATT TTT CAT GAT			1296
228	Ile Glu Ser Asp Asn Asn Phe Thr Asp Thr Thr Lys Ile Phe His Asp			
229	420	425	430	
230				
231	TCA TTA TTT AAT TCA GCT ACC GCA GAA AAC TCT ATG TTT TTA ACA AAA			1344
232	Ser Leu Phe Asn Ser Ala Thr Ala Glu Asn Ser Met Phe Leu Thr Lys			
233	435	440	445	
234				
235	ATA GCA CCA TAC TTA CAA GTA GGT TTT ATG CCA GAA GCT CGC TCC ACA			1392
236	Ile Ala Pro Tyr Leu Gln Val Gly Phe Met Pro Glu Ala Arg Ser Thr			
237	450	455	460	
238				
239	ATA AGT TTA AGT GGT CCA GGA GCT TAT GCG TCA GCT TAC TAT GAT TTC			1440
240	Ile Ser Leu Ser Gly Pro Gly Ala Tyr Ala Ser Ala Tyr Tyr Asp Phe			
241	465	470	475	480
242				
243	ATA AAT TTA CAA GAA AAT ACT ATA GAA AAA ACT TTA AAA GCA TCA GAT			1488
244	Ile Asn Leu Gln Glu Asn Thr Ile Glu Lys Thr Leu Lys Ala Ser Asp			
245	485	490	495	
246				
247	TTA ATA GAA TTT AAA TTC CCA GAA AAT AAT CTA TCT CAA TTG ACA GAA			1536
248	Leu Ile Glu Phe Lys Phe Pro Glu Asn Asn Leu Ser Gln Leu Thr Glu			
249	500	505	510	
250				
251	CAA GAA ATA AAT AGT CTA TGG AGC TTT GAT CAA GCA AGT GCA AAA TAT			1584
252	Gln Glu Ile Asn Ser Leu Trp Ser Phe Asp Gln Ala Ser Ala Lys Tyr			
253	515	520	525	
254				
255	CAA TTT GAG AAA TAT GTA AGA GAT TAT ACT GGT GGA TCT CTT TCT GAA			1632
256	Gln Phe Glu Lys Tyr Val Arg Asp Tyr Thr Gly Gly Ser Leu Ser Glu			
257	530	535	540	
258				